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RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/755,456

TIME: 11:59:14

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3 <110> APPLICANT: DELBAC, FREDERIC
4   DANCHIN, ANTOINE
5   VIVARES, CHRISTIAN
7 <120> TITLE OF INVENTION: MICROSPORIDIAN POLAR TUBE PROTEINS, NUCLEIC ACIDS
8   CODING FOR THESE PROTEINS AND THEIR APPLICATIONS
10 <130> FILE REFERENCE: 1566-00
12 <140> CURRENT APPLICATION NUMBER: 09/755,456
13 <141> CURRENT FILING DATE: 2001-01-05
15 <150> PRIOR APPLICATION NUMBER: PCT/FR99/01630
16 <151> PRIOR FILING DATE: 1999-07-06
18 <150> PRIOR APPLICATION NUMBER: FR 98/08692
19 <151> PRIOR FILING DATE: 1998-07-07
21 <160> NUMBER OF SEQ ID NOS: 10
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1830
27 <212> TYPE: DNA
28 <213> ORGANISM: Encephalitozoon cuniculi
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31 <221> NAME/KEY: CDS
32 <222> LOCATION: (345)..(1529)
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39 ggaggtgtct tggatggaaa gtaaggccat ttgtgggttc tcattccatgt catcgccct 180
41 ttcggctgtt tcaccaagat ccaattattc ctccaggact ttcaaccctc agaatggaaa 240
43 cagagatgaa actctctgtg caaatcgtag atatcgattg gagacattga aaccacggag 300
45 ttgaaataa aagtataaat acctccgaaa acgcagagtt taag atg aaa ggt att 356
46                                     Met Lys Gly Ile
47                                     1
49 tct aag atc ctc tct gcc tct att gcc ctg atg aag ttg gag aat gtc 404
50 Ser Lys Ile Leu Ser Ala Ser Ile Ala Leu Met Lys Leu Glu Asn Val
51   5          10          15          20
53 tat tca gca acc gca ctg tgc agc aat gca tat ggc cta act ccg gga 452
54 Tyr Ser Ala Thr Ala Leu Cys Ser Asn Ala Tyr Gly Leu Thr Pro Gly
55          25          30          35
57 caa cag ggt atg gct cag cag ccg tcg tat gtg ctg atc ccc agc acc 500
58 Gln Gln Gly Met Ala Gln Gln Pro Ser Tyr Val Leu Ile Pro Ser Thr
59          40          45          50
61 ccg gga acc ata gca aac tgt gca agc ggt tca cag gac aca tat tct 548
62 Pro Gly Thr Ile Ala Asn Cys Ala Ser Gly Ser Gln Asp Thr Tyr Ser
63          55          60          65
65 cct tct ccc gct gca ccc aca tct cca gtg act ccg ggg aaa act agc 596
66 Pro Ser Pro Ala Ala Pro Thr Ser Pro Val Thr Pro Gly Lys Thr Ser
67          70          75          80
69 gag aat gag aca tct cca tcg gct cct gca gaa gat gta gga aca tgc 644
70 Glu Asn Glu Thr Ser Pro Ser Ala Pro Ala Glu Asp Val Gly Thr Cys

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74	Lys	Ile	Ala	Val	Leu	Lys	His	Cys	Asp	Ala	Pro	Gly	Thr	Thr	Ser	Gly	
75					105					110					115		
77	acg	aca	cca	ggg	tca	ggg	cct	tgt	gaa	acc	cca	gag	cag	caa	cag	cct	740
78	Thr	Thr	Pro	Gly	Ser	Gly	Pro	Cys	Glu	Thr	Pro	Glu	Gln	Gln	Gln	Pro	
79				120					125					130			
81	ttg	tca	gtg	atc	tcc	acc	act	cct	gcc	gta	ccg	gtg	act	gtg	gag	tct	788
82	Leu	Ser	Val	Ile	Ser	Thr	Thr	Pro	Ala	Val	Pro	Val	Thr	Val	Glu	Ser	
83			135					140					145				
85	gca	cag	tct	cca	tct	gtt	gtg	cca	gtt	gtt	cct	gtc	gtt	gct	cac	cac	836
86	Ala	Gln	Ser	Pro	Ser	Val	Val	Pro	Val	Val	Pro	Val	Val	Ala	His	His	
87		150					155					160					
89	cag	gca	gtt	cca	ggc	tac	tac	aac	aat	gga	aca	tcc	ggt	att	cct	gga	884
90	Gln	Ala	Val	Pro	Gly	Tyr	Tyr	Asn	Asn	Gly	Thr	Ser	Gly	Ile	Pro	Gly	
91	165					170				175				180			
93	cag	caa	cag	atc	ctt	tct	ggc	act	ctt	ccc	cca	gga	gcc	act	ttg	tgt	932
94	Gln	Gln	Gln	Ile	Leu	Ser	Gly	Thr	Leu	Pro	Pro	Gly	Ala	Thr	Leu	Cys	
95				185					190					195			
97	cag	gga	cag	gcc	atg	cct	agc	act	cct	gga	cag	caa	cag	atc	ctt	tct	980
98	Gln	Gly	Gln	Ala	Met	Pro	Ser	Thr	Pro	Gly	Gln	Gln	Gln	Ile	Leu	Ser	
99			200					205					210				
101	ggc	act	ctt	ccc	cca	ggg	gtc	act	ttg	tgt	cag	gga	cag	gcc	acg	cct	1028
102	Gly	Thr	Leu	Pro	Pro	Gly	Val	Thr	Leu	Cys	Gln	Gly	Gln	Ala	Thr	Pro	
103			215					220				225					
105	agc	act	cct	ggg	cag	caa	cag	gtc	ctt	tct	ggc	act	ctt	ccc	cca	gga	1076
106	Ser	Thr	Pro	Gly	Gln	Gln	Gln	Val	Leu	Ser	Gly	Thr	Leu	Pro	Pro	Gly	
107		230				235					240						
109	gtc	act	ttg	tgt	cag	gga	cag	gcc	acg	cct	agc	act	cct	ggg	cag	caa	1124
110	Val	Thr	Leu	Cys	Gln	Gly	Gln	Ala	Thr	Pro	Ser	Thr	Pro	Gly	Gln	Gln	
111	245				250				255				260				
113	cag	gtc	ctt	tct	ggc	acc	ctt	ctc	cca	gga	gcc	act	ttg	tgt	cag	gat	1172
114	Gln	Val	Leu	Ser	Gly	Thr	Leu	Leu	Pro	Gly	Ala	Thr	Leu	Cys	Gln	Asp	
115			265					270				275					
117	caa	ggt	atg	cct	gga	aca	tcc	gga	gtt	cct	gga	cag	cag	gga	cag	tct	1220
118	Gln	Gly	Met	Pro	Gly	Thr	Ser	Gly	Val	Pro	Gly	Gln	Gln	Gly	Gln	Ser	
119			280					285				290					
121	agt	gga	cag	tgt	tgt	gcc	cct	cag	att	cca	aac	cct	gtc	atg	ccg	cca	1268
122	Ser	Gly	Gln	Cys	Cys	Ala	Pro	Gln	Ile	Pro	Asn	Pro	Val	Met	Pro	Pro	
123			295					300				305					
125	tcc	atg	aac	att	agt	gga	aat	ggg	tat	cct	tct	tct	acc	gca	tac	agc	1316
126	Ser	Met	Asn	Ile	Ser	Gly	Asn	Gly	Tyr	Pro	Ser	Ser	Thr	Ala	Tyr	Ser	
127		310				315				320							
129	cca	aac	ctc	gga	tca	ctg	gga	tcc	tgt	gtt	gac	ata	cag	aag	acg	ggg	1364
130	Pro	Asn	Leu	Gly	Ser	Leu	Gly	Ser	Cys	Val	Asp	Ile	Gln	Lys	Thr	Gly	
131	325				330				335				340				
133	ggg	aca	tcc	tgc	gag	caa	aaa	ccc	gag	aag	tcc	gcc	acg	cag	tat	gcc	1412
134	Gly	Thr	Ser	Cys	Glu	Gln	Lys	Pro	Glu	Lys	Ser	Ala	Thr	Gln	Tyr	Ala	
135				345				350				355					

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137 atg gag gcc tgt gca aca cca aca cca acg gtt att ata ggc aac agc 1460
138 Met Glu Ala Cys Ala Thr Pro Thr Pro Thr Val Ile Ile Gly Asn Ser
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141 gag tat ctt gtt gga cca gga atg tac aat gca att aac tct cca tgc 1508
142 Glu Tyr Leu Val Gly Pro Gly Met Tyr Asn Ala Ile Asn Ser Pro Cys
143          375          380          385
145 aac act gct gtc caa tgc tgc taggctaaaa taaaacgagt ttaatcttct 1559
146 Asn Thr Ala Val Gln Cys Cys
147          390          395
149 ttttcttcgg tcttttggaa cgttggatgg ggatggagga gtctatgggc tgaagtgaag 1619
151 tgccaacact tcttctgccc aagaacacat tcggatgttc ttctgtggc caggagtttg 1679
153 gtaacaggat tccccgagga tttagcagcc ttggagtacc atgattgaat cagtattaaa 1739
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166 <221> NAME/KEY: CDS
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174 gcattccataa tatatacaag acattccagg ctgcaactga atcaacacac tccatcccct 180
176 caggaagtcg gtaaaacttc cttgaaaata gccaatggat gtctccaggc ttataccat 240
178 gcacagctat atcttggcct gaagtgcact ttcagggtggg gctttgttac attgcgggtgt 300
180 tttggattac ctgatataat ttgttaccga ctgagtcaag tcgaaaccag tagtccgcag 360
182 atttctaaca gagaggaaag actggaggta atttgtggct ttgaaacat gcacagcaaa 420
184 ataaaaatata aaagaagcct ttgacacact accaaag atg ttg tta ctt ctc gcc 475
185                                     Met Leu Leu Leu Leu Ala
186                                     1           5
188 ata act gct gtt gtt agc gcc acg atg gtc cat cct tca gct gtt gtt 523
189 Ile Thr Ala Val Val Ser Ala Thr Met Val His Pro Ser Ala Val Val
190          10          15          20
192 cca cag ccc gca gca cct ctc cat gtc gtt ccc cca cag cag caa atg 571
193 Pro Gln Pro Ala Ala Pro Leu His Val Val Pro Pro Gln Gln Gln Met
194          25          30          35
196 ggc atg gtt aac gga tgc acc agc aag aaa cta gag ggt gca gaa ata 619
197 Gly Met Val Asn Gly Cys Thr Ser Lys Lys Leu Glu Gly Ala Glu Ile
198          40          45          50
200 atg aga agg aac atg att gag tgc cag aaa aga agc tcg gag gca aca 667
201 Met Arg Arg Asn Met Ile Glu Cys Gln Lys Arg Ser Ser Glu Ala Thr
202          55          60          65          70
204 aag gcg atg att gaa agg gca aat gaa aag gct gta gaa tca ttc aac 715
205 Lys Ala Met Ile Glu Arg Ala Asn Glu Lys Ala Val Glu Ser Phe Asn
206          75          80          85
208 aag gaa gtt agc aaa gga cct agc caa aag gat gga ggc cag tgc ata 763
209 Lys Glu Val Ser Lys Gly Pro Ser Gln Lys Asp Gly Gly Gln Cys Ile

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214          105          110          115
216 gat aag gcg gtg aac aag cgc aag tac aga atc tca gat gtg gag aac 859
217 Asp Lys Ala Val Asn Lys Arg Lys Tyr Arg Ile Ser Asp Val Glu Asn
218          120          125          130
220 agc acc tcg ctc tac aga gga gac aag cta att gcc cta att gtc aat 907
221 Ser Thr Ser Leu Tyr Arg Gly Asp Lys Leu Ile Ala Leu Ile Val Asn
222 135          140          145          150
224 gtc gac tat ggg ctg cag ccg atc act aag cca aag aag aag aag tcc 955
225 Val Asp Tyr Gly Leu Gln Pro Ile Thr Lys Pro Lys Lys Lys Ser
226          155          160          165
228 aag ata atg gcg aat ctc cct cag ccg aag aga gag atg tat ttc aac 1003
229 Lys Ile Met Ala Asn Leu Pro Gln Pro Lys Arg Glu Met Tyr Phe Asn
230          170          175          180
232 caa atc ggt cag ctt gtt gga gca aga gga acg ttc ccc cag gaa aac 1051
233 Gln Ile Gly Gln Leu Val Gly Ala Arg Gly Thr Phe Pro Gln Glu Asn
234          185          190          195
236 aag gag gac tgc aag cct tgt gag ggt ccc aag aag act gtt gaa act 1099
237 Lys Glu Asp Cys Lys Pro Cys Glu Gly Pro Lys Lys Thr Val Glu Thr
238          200          205          210
240 act tct gag aaa tgt aat ctt ggg tgc gag ctt aaa gga aca tct gct 1147
241 Thr Ser Glu Lys Cys Asn Leu Gly Cys Glu Leu Lys Gly Thr Ser Ala
242 215          220          225          230
244 ctg ata agc aag gcc ata cag aag aag gaa gtc aag gac acg aag gaa 1195
245 Leu Ile Ser Lys Ala Ile Gln Lys Lys Glu Val Lys Asp Thr Lys Glu
246          235          240          245
248 ggg gag aaa agt gca agc cag gac tct gat ggc gag ggc act gct gag 1243
249 Gly Glu Lys Ser Ala Ser Gln Asp Ser Asp Gly Glu Gly Thr Ala Glu
250          250          255          260
252 gat gcg gaa gta cag caa cct tct gcg gac ggc gag ggt cta gag 1288
253 Asp Ala Glu Val Gln Gln Pro Ser Ala Asp Gly Glu Gly Leu Glu
254          265          270          275
256 taatttttaa attaaaatct ccctggattg aatcttcaag tgcttttgtg aaagactttg 1348
258 ggaacatttc gtgaaggcta acataaattg ttaatctcag gtcactcgat ggaatagtca 1408
260 attcgatttt cctttccttg gatggtctgc cccaccagcc tgttcctggc agttatcgca 1468
262 tcgtcgacag agtcaaaactg aacgaatcca tatcctttgg acatcttctt gtattggtcg 1528
264 tagactatta ctaccgata gttcagtatc tcactgatcc tctccttgag aaggtctcta 1588
266 acgtcgtctt cggttatgtg tgctccagc ccaaatatcc ctatcgccct ggaggagac 1648
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276 <213> ORGANISM: Encephalitozoon intestinalis
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287 ttg aag ggt gtc tat tct aca act gtg ctg tgt gga gat tca aca caa 96
288 Leu Lys Gly Val Tyr Ser Thr Thr Val Leu Cys Gly Asp Ser Thr Gln
289 20 25 30
291 gga ctg cag ggc aca acc caa ccg tca tat gtg ctg gtt cct agt gca 144
292 Gly Leu Gln Gly Thr Thr Gln Pro Ser Tyr Val Leu Val Pro Ser Ala
293 35 40 45
295 cca gag aca ata gcc aac tgt gga tac agt cca cag aac atg tat gtc 192
296 Pro Glu Thr Ile Ala Asn Cys Gly Tyr Ser Pro Gln Asn Met Tyr Val
297 50 55 60
299 cct tct act cct act acc atg cct tcc aca gtg cca ggc aca act ggt 240
300 Pro Ser Thr Pro Thr Thr Met Pro Ser Thr Val Pro Gly Thr Thr Gly
301 65 70 75 80
303 gag agc gag aca cct act tct cca aca tca tct cct aca gag gat gtg 288
304 Glu Ser Glu Thr Pro Thr Ser Pro Thr Ser Ser Pro Thr Glu Asp Val
305 85 90 95
307 gga aca tgc aag att gct gtt gta aag cat tgt gat gca cca gga aca 336
308 Gly Thr Cys Lys Ile Ala Val Val Lys His Cys Asp Ala Pro Gly Thr
309 100 105 110
311 tca tca aca cct tgc gaa ccg gaa cag act ttg gcc ccc tct cag cca 384
312 Ser Ser Thr Pro Cys Glu Pro Glu Gln Thr Leu Ala Pro Ser Gln Pro
313 115 120 125
315 gta gca gct aca att gcc aca cca ctg gtt gtt gct tct gtg cag acg 432
316 Val Ala Ala Thr Ile Ala Thr Pro Leu Val Val Ala Ser Val Gln Thr
317 130 135 140
319 ccg caa gca gct gtt acc atc ctt act cca aag gcc gtc tct gcc cag 480
320 Pro Gln Ala Ala Val Thr Ile Leu Thr Pro Lys Ala Val Ser Ala Gln
321 145 150 155 160
323 ccg gca acc atc att tct cca ttc aac cag gca cca ggc tac tac aat 528
324 Pro Ala Thr Ile Ile Ser Pro Phe Asn Gln Ala Pro Gly Tyr Tyr Asn
325 165 170 175
327 agt gca att ccc ggg caa ata ctt aca ggt aat gtt ctc tct cca agt 576
328 Ser Ala Ile Pro Gly Gln Ile Leu Thr Gly Asn Val Leu Ser Pro Ser
329 180 185 190
331 gcc tct tct tgc caa gtg gtg ccc gga aca aca gga agc tcc acc ccc 624
332 Ala Ser Ser Cys Gln Val Val Pro Gly Thr Thr Gly Ser Ser Thr Pro
333 195 200 205
335 cag cag cta cca ggc gct gtt tca tct gga acc att cct tgc caa ata 672
336 Gln Gln Leu Pro Gly Ala Val Ser Ser Gly Thr Ile Pro Cys Gln Ile
337 210 215 220
339 gta cag gga act caa agt agc gga aac acc cct gga cag caa ttc ttg 720
340 Val Gln Gly Thr Gln Ser Ser Gly Asn Thr Pro Gly Gln Gln Phe Leu
341 225 230 235 240
343 ccg gga atc gtt cct gtt gga agc ctc cag ccg gat caa gct act tct 768
344 Pro Gly Ile Val Pro Val Gly Ser Leu Gln Pro Asp Gln Ala Thr Ser
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